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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/990,578

DATE: 11/28/2001

TIME: 10:36:26

Input Set : A:\TAMK232.ST25.txt

Output Set: N:\CRF3\11212001\I990578.raw

ENTERED

3 <110> APPLICANT: McKeehan, Wallace L.  
 4 Luo, Yongde  
 6 <120> TITLE OF INVENTION: FGF-Affinity Chromatography  
 8 <130> FILE REFERENCE: 12740.0232.NPUS00 TAMK:232  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/990,578  
 C--> 10 <141> CURRENT FILING DATE: 2001-11-21  
 10 <150> PRIOR APPLICATION NUMBER: US 60/325,613  
 11 <151> PRIOR FILING DATE: 2001-09-28  
 13 <150> PRIOR APPLICATION NUMBER: US 60/325,502  
 14 <151> PRIOR FILING DATE: 2001-08-28  
 16 <150> PRIOR APPLICATION NUMBER: US 60/277,735  
 17 <151> PRIOR FILING DATE: 2001-03-21  
 19 <150> PRIOR APPLICATION NUMBER: US 60/252,225  
 20 <151> PRIOR FILING DATE: 2000-11-21  
 22 <160> NUMBER OF SEQ ID NOS: 4  
 24 <170> SOFTWARE: PatentIn version 3.1  
 26 <210> SEQ ID NO: 1  
 27 <211> LENGTH: 693  
 28 <212> TYPE: DNA  
 29 <213> ORGANISM: FGF7 from Rat  
 31 <220> FEATURE:  
 32 <221> NAME/KEY: CDS  
 33 <222> LOCATION: (109)..(693)  
 34 <223> OTHER INFORMATION: Full length DNA sequence for FGF7  
 36 <400> SEQUENCE: 1  
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 39 tccagttctc attatgttat tcatggacac ccggggcact gctctata atg cgc aaa 117  
 40 Met Arg Lys  
 41 1  
 43 tgg ata ctg aca cgg atc ctg ccg act ccg ctc tac aga ccg tgc ttc 165  
 44 Trp Ile Leu Thr Arg Ile Leu Pro Thr Pro Leu Tyr Arg Pro Cys Phe  
 45 5 10 15  
 47 cac ctc gtc tgt ctt gtg ggc acc ata tct tta gct tgc aat gac atg 213  
 48 His Leu Val Cys Leu Val Gly Thr Ile Ser Leu Ala Cys Asn Asp Met  
 49 20 25 30 35  
 51 agt cca gag cag acg gcc acg agc gtg aac tgt tct agc ccc gag cga 261  
 52 Ser Pro Glu Gln Thr Ala Thr Ser Val Asn Cys Ser Ser Pro Glu Arg  
 53 40 45 50  
 55 cac acg aga agt tat gac tac atg gaa gga ggg gat ata agg gtg agg 309  
 56 His Thr Arg Ser Tyr Asp Tyr Met Glu Gly Gly Asp Ile Arg Val Arg  
 57 55 60 65  
 59 aga ctg ttc tgt cgc acc cag tgg tac ctg agg att gac aaa cga ggc 357  
 60 Arg Leu Phe Cys Arg Thr Gln Trp Tyr Leu Arg Ile Asp Lys Arg Gly  
 61 70 75 80  
 63 aaa gtg aaa ggg acc cag gag atg agg aac agc tac aac atc atg gaa 405  
 64 Lys Val Lys Gly Thr Gln Glu Met Arg Asn Ser Tyr Asn Ile Met Glu  
 65 85 90 95

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67 atc atg act gtg gca gtt gga att gtg gca atc aaa ggg gtg gaa agt      453
68 Ile Met Thr Val Ala Val Gly Ile Val Ala Ile Lys Gly Val Glu Ser
69 100                               105                               110                               115
71 gaa tac tat ctt gcc atg aac aaa caa ggg gaa ctc tat gca aag aaa
72 Glu Tyr Tyr Leu Ala Met Asn Lys Gln Gly Glu Leu Tyr Ala Lys Lys      501
73                               120                               125                               130
75 gaa tgc aat gag gat tgc aac ttc aaa gaa ctg att ctg gaa aac cat
76 Glu Cys Asn Glu Asp Cys Asn Phe Lys Glu Leu Ile Leu Glu Asn His      549
77                               135                               140                               145
79 tac aac acc tct gca tca gct aaa tgg aca cac agc gga ggg gaa atg
80 Tyr Asn Thr Ser Ala Ser Ala Lys Trp Thr His Ser Gly Gly Glu Met      597
81                               150                               155                               160
83 ttc gtg gcc tta aat caa aag ggg ctt cct gtc aaa ggg aag aaa acg
84 Phe Val Ala Leu Asn Gln Lys Gly Leu Pro Val Lys Gly Lys Lys Thr      645
85                               165                               170                               175
87 aag aaa gaa caa aaa acg gcc cac ttt ctt cct atg gca ata act taa
88 Lys Lys Glu Gln Lys Thr Ala His Phe Leu Pro Met Ala Ile Thr      693
89 180                               185                               190
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93 <211> LENGTH: 194
94 <212> TYPE: PRT
95 <213> ORGANISM: FGF7 from Rat
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100 1                               5                               10                               15
102 Pro Cys Phe His Leu Val Cys Leu Val Gly Thr Ile Ser Leu Ala Cys
103                               20                               25                               30
105 Asn Asp Met Ser Pro Glu Gln Thr Ala Thr Ser Val Asn Cys Ser Ser
106                               35                               40                               45
108 Pro Glu Arg His Thr Arg Ser Tyr Asp Tyr Met Glu Gly Gly Asp Ile
109                               50                               55                               60
111 Arg Val Arg Arg Leu Phe Cys Arg Thr Gln Trp Tyr Leu Arg Ile Asp
112 65                               70                               75                               80
114 Lys Arg Gly Lys Val Lys Gly Thr Gln Glu Met Arg Asn Ser Tyr Asn
115                               85                               90                               95
117 Ile Met Glu Ile Met Thr Val Ala Val Gly Ile Val Ala Ile Lys Gly
118                               100                              105                              110
120 Val Glu Ser Glu Tyr Tyr Leu Ala Met Asn Lys Gln Gly Glu Leu Tyr
121                               115                              120                              125
123 Ala Lys Lys Glu Cys Asn Glu Asp Cys Asn Phe Lys Glu Leu Ile Leu
124                               130                              135                              140
126 Glu Asn His Tyr Asn Thr Ser Ala Ser Ala Lys Trp Thr His Ser Gly
127 145                              150                              155                              160
129 Gly Glu Met Phe Val Ala Leu Asn Gln Lys Gly Leu Pro Val Lys Gly
130                               165                               170                               175
132 Lys Lys Thr Lys Lys Glu Gln Lys Thr Ala His Phe Leu Pro Met Ala
133                               180                               185                               190
135 Ile Thr
138 <210> SEQ ID NO: 3

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139 <211> LENGTH: 1182
140 <212> TYPE: DNA
141 <213> ORGANISM: Artificial Sequence
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144 <223> OTHER INFORMATION: Synthetic
146 <220> FEATURE:
147 <221> NAME/KEY: CDS
148 <222> LOCATION: (1)..(1182)
149 <223> OTHER INFORMATION: Fusion protein GST-FGF7
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154 1 5 10 15
156 act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg      96
157 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu
158 20 25 30
160 tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg      144
161 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
162 35 40 45
164 ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa      192
165 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
166 50 55 60
168 tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac      240
169 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
170 65 70 75 80
172 atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa      288
173 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
174 85 90 95
176 gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt      336
177 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
178 100 105 110
180 aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa      384
181 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
182 115 120 125
184 atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat      432
185 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
186 130 135 140
188 ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat      480
189 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
190 145 150 155 160
192 gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta      528
193 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
194 165 170 175
196 gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac      576
197 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
198 180 185 190
200 ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc      624
201 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
202 195 200 205

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204 acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt
205 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg      672
206      210      215      220
208 gga tcc ccg cgg gaa ttc gct tgc aat gac atg agt cca gag cag acg
209 Gly Ser Pro Arg Glu Phe Ala Cys Asn Asp Met Ser Pro Glu Gln Thr      720
210 225      230      235      240
212 gcc acg agc gtg aac tgt tct agc ccc gag cga cac acg aga agt tat
213 Ala Thr Ser Val Asn Cys Ser Ser Pro Glu Arg His Thr Arg Ser Tyr      768
214      245      250      255
216 gac tac atg gaa gga ggg gat ata agg gtg agg aga ctg ttc tgt cgc
217 Asp Tyr Met Glu Gly Gly Asp Ile Arg Val Arg Arg Leu Phe Cys Arg      816
218      260      265      270
220 acc cag tgg tac ctg agg att gac aaa cga ggc aaa gtg aaa ggg acc
221 Thr Gln Trp Tyr Leu Arg Ile Asp Lys Arg Gly Lys Val Lys Gly Thr      864
222      275      280      285
224 cag gag atg agg aac agc tac aac atc atg gaa atc atg act gtg gca
225 Gln Glu Met Arg Asn Ser Tyr Asn Ile Met Glu Ile Met Thr Val Ala      912
226      290      295      300
228 gtt gga att gtg gca atc aaa ggg gtg gaa agt gaa tac tat ctt gcc
229 Val Gly Ile Val Ala Ile Lys Gly Val Glu Ser Glu Tyr Tyr Leu Ala      960
230 305      310      315      320
232 atg aac aaa caa ggg gaa ctc tat gca aag aaa gaa tgc aat gag gat
233 Met Asn Lys Gln Gly Glu Leu Tyr Ala Lys Lys Glu Cys Asn Glu Asp      1008
234      325      330      335
236 tgc aac ttc aaa gaa ctg att ctg gaa aac cat tac aac acc tct gca
237 Cys Asn Phe Lys Glu Leu Ile Leu Glu Asn His Tyr Asn Thr Ser Ala      1056
238      340      345      350
240 tca gct aaa tgg aca cac agc gga ggg gaa atg ttc gtg gcc tta aat
241 Ser Ala Lys Trp Thr His Ser Gly Gly Glu Met Phe Val Ala Leu Asn      1104
242      355      360      365
244 caa aag ggg ctt cct gtc aaa ggg aag aaa acg aag aaa gaa caa aaa
245 Gln Lys Gly Leu Pro Val Lys Gly Lys Lys Thr Lys Lys Glu Gln Lys      1152
246      370      375      380
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250 385      390      1182
252 <210> SEQ ID NO: 4
253 <211> LENGTH: 394
254 <212> TYPE: PRT
255 <213> ORGANISM: Artificial Sequence
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259 <400> SEQUENCE: 4
261 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
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264 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
265      20      25      30
267 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
268      35      40      45

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270 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
271      50                      55                      60
273 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
274 65                      70                      75                      80
276 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
277      85                      90                      95
279 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
280      100                     105                     110
282 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
283      115                     120                     125
285 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
286      130                     135                     140
288 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
289 145                     150                     155                     160
291 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
292      165                     170                     175
294 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
295      180                     185                     190
297 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
298      195                     200                     205
300 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
301      210                     215                     220
303 Gly Ser Pro Arg Glu Phe Ala Cys Asn Asp Met Ser Pro Glu Gln Thr
304 225                     230                     235                     240
306 Ala Thr Ser Val Asn Cys Ser Ser Pro Glu Arg His Thr Arg Ser Tyr
307      245                     250                     255
309 Asp Tyr Met Glu Gly Gly Asp Ile Arg Val Arg Arg Leu Phe Cys Arg
310      260                     265                     270
312 Thr Gln Trp Tyr Leu Arg Ile Asp Lys Arg Gly Lys Val Lys Gly Thr
313      275                     280                     285
315 Gln Glu Met Arg Asn Ser Tyr Asn Ile Met Glu Ile Met Thr Val Ala
316      290                     295                     300
318 Val Gly Ile Val Ala Ile Lys Gly Val Glu Ser Glu Tyr Tyr Leu Ala
319 305                     310                     315                     320
321 Met Asn Lys Gln Gly Glu Leu Tyr Ala Lys Lys Glu Cys Asn Glu Asp
322      325                     330                     335
324 Cys Asn Phe Lys Glu Leu Ile Leu Glu Asn His Tyr Asn Thr Ser Ala
325      340                     345                     350
327 Ser Ala Lys Trp Thr His Ser Gly Gly Glu Met Phe Val Ala Leu Asn
328      355                     360                     365
330 Gln Lys Gly Leu Pro Val Lys Gly Lys Lys Thr Lys Lys Glu Gln Lys
331      370                     375                     380
333 Thr Ala His Phe Leu Pro Met Ala Ile Thr
334 385                     390

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VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:256 M:283 W: Missing Blank Line separator, <220> field identifier